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<151> 1996-10-25

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<170> PatentIn Ver. 2.1

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ccaaccttca aagttcaagt agtgat atg gat gac tcc aca gaa agg gag cag 173
Met Asp Asp Ser Thr Glu Arg Glu Gln
1 5

tca cgc ctt act tct tgc ctt aag aaa aga gaa gaa atg aaa ctg aag 221
Ser Arg Leu Thr Ser Cys Leu Lys Lys Arg Glu Glu Met Lys Leu Lys
10 15 20 25

gag tgt gtt tcc atc ctc cca cgg aag gaa agc ccc tct gtc cga tcc 269
Glu Cys Val Ser Ile Leu Pro Arg Lys Glu Ser Pro Ser Val Arg Ser
30 35 40

tcc aaa gac gga aag ctg ctg gct gca acc ttg ctg ctg gca ctg ctg 317
Ser Lys Asp Gly Lys Leu Leu Ala Ala Thr Leu Leu Leu Ala Leu Leu
45 50 55

tct tgc tgc ctc acg gtg gtg tct ttc tac cag gtg gcc gcc ctg caa 365
Ser Cys Cys Leu Thr Val Val Ser Phe Tyr Gln Val Ala Ala Leu Gln
60 65 70

ggg gac ctg gcc agc ctc cgg gca gag ctg cag ggc cac cac gcg gag 413
Gly Asp Leu Ala Ser Leu Arg Ala Glu Leu Gln Gly His His Ala Glu
75 80 85

aag ctg cca gca gga gca gga gcc ccc aag gcc ggc ctg gag gaa gct 461
Lys Leu Pro Ala Gly Ala Gly Ala Pro Lys Ala Gly Leu Glu Glu Ala
90 95 100 105

347

C

C'
cont.

cca gct gtc acc gcg gga ctg aaa atc ttt gaa cca cca gct cca gga	509
Pro Ala Val Thr Ala Gly Leu Lys Ile Phe Glu Pro Pro Ala Pro Gly	
110 115 120	
gaa ggc aac tcc agt cag aac agc aga aat aag cgt gcc gtt cag ggt	557
Glu Gly Asn Ser Ser Gln Asn Ser Arg Asn Lys Arg Ala Val Gln Gly	
125 130 135	
cca gaa gaa aca gtc act caa gac tgc ttg caa ctg att gca gac agt	605
Pro Glu Glu Thr Val Thr Gln Asp Cys Leu Gln Leu Ile Ala Asp Ser	
140 145 150	
gaa aca cca act ata caa aaa gga tct tac aca ttt gtt cca tgg ctt	653
Glu Thr Pro Thr Ile Gln Lys Gly Ser Tyr Thr Phe Val Pro Trp Leu	
155 160 165	
ctc agc ttt aaa agg gga agt gcc cta gaa gaa aaa gag aat aaa ata	701
Leu Ser Phe Lys Arg Gly Ser Ala Leu Glu Glu Lys Glu Asn Lys Ile	
170 175 180 185	
ttg gtc aaa gaa act ggt tac ttt ttt ata tat ggt cag gtt tta tat	749
Leu Val Lys Glu Thr Gly Tyr Phe Phe Ile Tyr Gly Gln Val Leu Tyr	
190 195 200	
act gat aag acc tac gcc atg gga cat cta att cag agg aag aag gtc	797
Thr Asp Lys Thr Tyr Ala Met Gly His Leu Ile Gln Arg Lys Lys Val	
205 210 215	
cat gtc ttt ggg gat gaa ttg agt ctg gtg act ttg ttt cga tgt att	845
His Val Phe Gly Asp Glu Leu Ser Leu Val Thr Leu Phe Arg Cys Ile	
220 225 230	
caa aat atg cct gaa aca cta ccc aat aat tcc tgc tat tca gct ggc	893
Gln Asn Met Pro Glu Thr Leu Pro Asn Asn Ser Cys Tyr Ser Ala Gly	
235 240 245	
att gca aaa ctg gaa gaa gga gat gaa ctc caa ctt gca ata cca aga	941
Ile Ala Lys Leu Glu Glu Gly Asp Glu Leu Gln Leu Ala Ile Pro Arg	
250 255 260 265	
gaa aat gca caa ata tca ctg gat gga gat gtc aca ttt ttt ggt gca	989
Glu Asn Ala Gln Ile Ser Leu Asp Gly Asp Val Thr Phe Phe Gly Ala	
270 275 280	
ttg aaa ctg ctg tgacctactt acaccatgtc tgtagctatt ttctctcctt	1041
Leu Lys Leu Leu	
285	
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Met Asp Asp Ser Thr Glu Arg Glu Gln Ser Arg Leu Thr Ser Cys Leu

393

C

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Leu His Leu Leu Leu Leu Gly Leu Leu Leu Val Leu Leu Pro Gly Ala
      20             25             30

Gln Gly Leu Pro Gly Val Gly Leu Thr Pro Ser Ala Ala Gln Thr Ala
    35             40             45

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C

Arg Gln His Pro Lys Met His Leu Ala His Ser Thr Leu Lys Pro Ala
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 Ala His Leu Ile Gly Asp Pro Ser Lys Gln Asn Ser Leu Leu Trp Arg
 65 70 75 80
 Ala Asn Thr Asp Arg Ala Phe Leu Gln Asp Gly Phe Ser Leu Ser Asn
 85 90 95
 Asn Ser Leu Leu Val Pro Thr Ser Gly Ile Tyr Phe Val Tyr Ser Gln
 100 105 110
 Val Val Phe Ser Gly Lys Ala Tyr Ser Pro Lys Ala Thr Ser Ser Pro
 115 120 125
 Leu Tyr Leu Ala His Glu Val Gln Leu Phe Ser Ser Gln Tyr Pro Phe
 130 135 140
 His Val Pro Leu Leu Ser Ser Gln Lys Met Val Tyr Pro Gly Leu Gln
 145 150 155 160
 Glu Pro Trp Leu His Ser Met Tyr His Gly Ala Ala Phe Gln Leu Thr
 165 170 175
 Gln Gly Asp Gln Leu Ser Thr His Thr Asp Gly Ile Pro His Leu Val
 180 185 190
 Leu Ser Pro Ser Thr Val Phe Phe Gly Ala Phe Ala Leu
 195 200 205

C'
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 <213> Homo sapiens

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 Gly Ser Leu Leu Leu Ala Val Ala Gly Ala Thr Ser Leu Val Thr Leu
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 Leu Leu Ala Val Pro Ile Thr Val Leu Ala Val Leu Ala Leu Val Pro
 35 40 45
 Gln Asp Gln Gly Gly Leu Val Thr Glu Thr Ala Asp Pro Gly Ala Gln
 50 55 60
 Ala Gln Gln Gly Leu Gly Phe Gln Lys Leu Pro Glu Glu Glu Pro Glu
 65 70 75 80
 Thr Asp Leu Ser Pro Gly Leu Pro Ala Ala His Leu Ile Gly Ala Pro
 85 90 95
 Leu Lys Gly Gln Gly Leu Gly Trp Glu Thr Thr Lys Glu Gln Ala Phe
 100 105 110
 Leu Thr Ser Gly Thr Gln Phe Ser Asp Ala Glu Gly Leu Ala Leu Pro
 115 120 125

2010

C

Gln Asp Gly Leu Tyr Tyr Leu Tyr Cys Leu Val Gly Tyr Arg Gly Arg
 130 135 140
 Ala Pro Pro Gly Gly Gly Asp Pro Gln Gly Arg Ser Val Thr Leu Arg
 145 150 155 160
 Ser Ser Leu Tyr Arg Ala Gly Gly Ala Tyr Gly Pro Gly Thr Pro Glu
 165 170 175
 Leu Leu Leu Glu Gly Ala Glu Thr Val Thr Pro Val Leu Asp Pro Ala
 180 185 190
 Arg Arg Gln Gly Tyr Gly Pro Leu Trp Tyr Thr Ser Val Gly Phe Gly
 195 200 205
 Gly Leu Val Gln Leu Arg Arg Gly Glu Arg Val Tyr Val Asn Ile Ser
 210 215 220
 His Pro Asp Met Val Asp Phe Ala Arg Gly Lys Thr Phe Phe Gly Ala
 225 230 235 240
 Val Met Val Gly

<210> 6
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 a, t, g, or c

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 Ser Ser Ala Ser Ser Pro Trp Ala Pro Pro Gly Thr Val Leu Pro Cys
 20 25 30
 Pro Thr Ser Val Pro Arg Arg Pro Gly Gln Arg Arg Pro Pro Pro Pro
 35 40 45
 Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro Pro Leu Pro
 50 55 60
 Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg Gly Asn His Ser Thr Gly
 65 70 75 80
 Leu Cys Leu Leu Val Met Phe Phe Met Val Leu Val Ala Leu Val Gly
 85 90 95
 Leu Gly Leu Gly Met Phe Gln Leu Phe His Leu Gln Lys Glu Leu Ala
 100 105 110
 Glu Leu Arg Glu Ser Thr Ser Gln Met His Thr Ala Ser Ser Leu Glu
 115 120 125

Lys Gln Ile Gly His Pro Ser Pro Pro Pro Glu Lys Lys Glu Leu Arg
 130 135 140
 Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg Ser Met Pro Leu
 145 150 155 160
 Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly Val Lys Tyr
 165 170 175
 Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr
 180 185 190
 Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Leu Pro Leu Ser
 195 200 205
 His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln Asp Leu Val Met
 210 215 220
 Met Glu Gly Lys Met Met Ser Tyr Cys Thr Thr Gly Gln Met Trp Ala
 225 230 235 240
 Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala Asp His
 245 250 255
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tcaaagttca agtagtgata tggatgactc cacagaaagg gagcagtcac gccttacttc 180
ttgccttaag aaaagagaag aaatgaaact gnaaggagtg tgtttccatc ctcccacgga 240
aggaaagccc ctctntccga tcctccaaag acggaaagct gctggctgca accttgntgn 300
tggcattgtg ttcttgctgn ctcaaggtgg tgttntt 337

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agtctggtga ctttgtttcg atgtattcaa aatatgcctg aaacactacc caataattcc 180
tgctattcag ctggcattgc aaaactggna ggaaggagat gaactccaac ttgcaatacc 240
aggggaaaaat gcacaattat cactgggatg gagatgttca cattttttgg gtgccattga 300
aactgctgtg acctncttac ancangtget gttngctatt ttncctnct nttctntggt 360
aacctcttag gaaggaagga ttcttaactg ggaaataacc caaaaaaann ttaaangggg 420
angngnnana ngnggggngg ttncnngnn gnnttttngg nntatntnt nntnggggnn 480
ngtaaaaatg gggccnangg gggnttttt 509

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ccgttcaggg tccagaagaa acagtcactc aagactgctt gcaactgntt gcagacagtg 180
aaacaccaac tatacaaaaa ggctcccttc tgntgccaca tttgggcca ggaatggaga 240
gattttcttcg tctggaaaca ttttgccaaa ctcttcagat actcttttct ctctgggaat 300
caaaggaaaa tctctactta gattnacaca tttgttccca tgggtntctt aagtttttaa 360
aggggagtg ccttaggagg aaaaggggat aaatattggc caaggnactg gttantttnt 420
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<210> 11
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<223> primer

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<210> 13
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28

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ctggggctgc tcttggtgtt gcctgctgcc ttccctgccc cagttgtgag acaaggggac 120
ctggccagc 129

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1 5 10 15
aag aaa aga gaa gaa atg aaa ctg aag gag tgt gtt tcc atc ctc cca 96
Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro
20 25 30
cgg aag gaa agc ccc tct gtc cga tcc tcc aaa gac gga aag ctg ctg 144
Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu
35 40 45
gct gca acc ttg ctg ctg gca ctg ctg tct tgc tgc ctc acg gtg gtg 192
Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val
50 55 60
tct ttc tac cag gtg gcc gcc ctg caa ggg gac ctg gcc agc ctc cgg 240
Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
65 70 75 80
gca gag ctg cag ggc cac cac gcg gag aag ctg cca gca gga gca gga 288
Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly
85 90 95
gcc ccc aag gcc ggc ctg gag gaa gct cca gct gtc acc gcg gga ctg 336
Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
100 105 110
aaa atc ttt gaa cca cca gct cca gga gaa ggc aac tcc agt cag aac 384
Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
115 120 125
agc aga aat aag cgt gcc gtt cag ggt cca gaa gaa aca gga tct tac 432
Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Gly Ser Tyr
130 135 140
aca ttt gtt cca tgg ctt ctc agc ttt aaa agg gga agt gcc cta gaa 480
Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu Glu
145 150 155 160
gaa aaa gag aat aaa ata ttg gtc aaa gaa act ggt tac ttt ttt ata 528
Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe Ile

165	170	175	
tat ggt cag gtt tta tat act gat aag acc tac gcc atg gga cat cta			576
Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His Leu			
180	185	190	
att cag agg aag aag gtc cat gtc ttt ggg gat gaa ttg agt ctg gtg			624
Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu Val			
195	200	205	
act ttg ttt cga tgt att caa aat atg cct gaa aca cta ccc aat aat			672
Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn Asn			
210	215	220	
tcc tgc tat tca gct ggc att gca aaa ctg gaa gaa gga gat gaa ctc			720
Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu Leu			
225	230	235	240
caa ctt gca ata cca aga gaa aat gca caa ata tca ctg gat gga gat			768
Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly Asp			
245	250	255	
gtc aca ttt ttt ggt gca ttg aaa ctg ctg tgacctactt acaccatgtc			818
Val Thr Phe Phe Gly Ala Leu Lys Leu Leu			
260	265		
tgtagctatt ttcctccctt tctctgtacc tctaagaaga aagaatctaa ctgaaaatac			878
caaaaaaaaaa aaaaaaaaaa aaaaaa			903

C' cont.
 <210> 19
 <211> 266
 <212> PRT
 <213> Homo sapiens

<400> 19
 Met Asp Asp Ser Thr Glu Arg Glu Gln Ser Arg Leu Thr Ser Cys Leu
 1 5 10 15
 Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro
 20 25 30
 Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu
 35 40 45
 Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val
 50 55 60
 Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
 65 70 75 80
 Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly
 85 90 95
 Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
 100 105 110
 Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
 115 120 125

Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Gly Ser Tyr
 130 135 140
 Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu Glu
 145 150 155 160
 Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe Ile
 165 170 175
 Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His Leu
 180 185 190
 Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu Val
 195 200 205
 Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn Asn
 210 215 220
 Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu Leu
 225 230 235 240
 Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly Asp
 245 250 255
 Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
 260 265

<210> 20
 <211> 136
 <212> PRT
 <213> Homo sapiens

<400> 20
 His Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser Lys Asp Asp
 1 5 10 15
 Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg Arg Gly Arg
 20 25 30
 Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala Gly Val
 35 40 45
 Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe Thr Met
 50 55 60
 Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr Leu Phe
 65 70 75 80
 Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr Asn Ser
 85 90 95
 Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp Ile Leu Ser
 100 105 110
 Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser Pro His Gly
 115 120 125

Thr Phe Leu Gly Phe Val Lys Leu
130 135

<210> 21
<211> 462
<212> DNA
<213> Homo sapiens

<400> 21
atggctgttc aggggtccgga agaaaccggt actcaggact gccttcagct gatcgcagac 60
tctgaaactc cgaccatcca gaaagggttct tacacctttg ttccttggct gctttctttc 120
aaacgtgggt ctgccctgga agagaaagaa aacaaaatcc tggttaaaga aactgggttac 180
ttctttatct acggtcaggt tctttacact gataagacct acgccatggg tcacctgatt 240
cagcgttaaga aagttcacgt ttccgggtgac gagctgtctc tggttactct gtttcgctgc 300
attcagaaca tgccggaaac tcttcctaac aactcctgct actctgctgg catcgcaaaa 360
ctggaagagg gtgatgaact gcagctggca attcctcgtg aaaacgcaca aatttctctg 420
gacgggtgatg taaccttctt tgggtgcactg aaacttctgt aa 462

<210> 22
<211> 1040
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(468)

<400> 22
cgc gtg gta gac ctc tca gct cct cct gca cca tgc ctg cct gga tgc 48
Arg Val Val Asp Leu Ser Ala Pro Pro Ala Pro Cys Leu Pro Gly Cys
1 5 10 15
cgc cat tct caa cat gat gat aat gga atg aac ctc aga aac aga act 96
Arg His Ser Gln His Asp Asp Asn Gly Met Asn Leu Arg Asn Arg Thr
20 25 30
tac aca ttt gtt cca tgg ctt ctc agc ttt aaa aga gga aat gcc ttg 144
Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Asn Ala Leu
35 40 45
gag gag aaa gag aac aaa ata gtg gtg agg caa aca ggc tat ttc ttc 192
Glu Glu Lys Glu Asn Lys Ile Val Val Arg Gln Thr Gly Tyr Phe Phe
50 55 60
atc tac agc cag gtt cta tac acg gac ccc atc ttt gct atg ggt cat 240
Ile Tyr Ser Gln Val Leu Tyr Thr Asp Pro Ile Phe Ala Met Gly His
65 70 75 80
gtc atc cag agg aag aaa gta cac gtc ttt ggg gac gag ctg agc ctg 288
Val Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu
85 90 95
gtg acc ctg ttc cga tgt att cag aat atg ccc aaa aca ctg ccc aac 336
Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Lys Thr Leu Pro Asn
100 105 110
aat tcc tgc tac tgc gct ggc atc gcg agg ctg gaa gaa gga gat gag 384
Asn Ser Cys Tyr Ser Ala Gly Ile Ala Arg Leu Glu Glu Gly Asp Glu

115

120

125

att cag ctt gca att cct cgg gag aat gca cag att tca cgc aac gga 432
 Ile Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Arg Asn Gly
 130 135 140

gac gac acc ttc ttt ggt gcc cta aaa ctg ctg taa ctcacttgct 478
 Asp Asp Thr Phe Phe Gly Ala Leu Lys Leu Leu
 145 150 155

ggagtgcgtg atcccccttcc ctcgctcttct ctgtacctcc gagggagaaa cagacgactg 538
 gaaaaactaa aagatgggga aagccgtcag cgaaagtttt ctcgtgaccc gttgaatctg 598
 atccaaacca ggaaatataa cagacagcca caaccgaagt gtgccatgtg agttatgaga 658
 aacggagccc gcgctcagaa agaccggatg aggaagaccg ttttctccag tcctttgcca 718
 acacgcaccg caaccttgct ttttgcttg ggtgacacat gttcagaatg cagggagatt 778
 tccttgTTTT gcgatttgcc atgagaagag ggcccacaac tgcaggtcac tgaagcattc 838
 acgctaagtc tcaggattta ctctcccttc tcatgctaag tacacacacg ctctttttcca 898
 ggtaatacta tgggatacta tggaaagggt gtttgTTTT aaatctagaa gtcttgaact 958
 ggcaatagac aaaaatcctt ataaattcaa gtgtaaaata aacttaatta aaaagggttta 1018
 agtgtgaaaa aaaaaaaaaa aa 1040

<210> 23

<211> 155

<212> PRT

<213> Homo sapiens

<400> 23

Arg Val Val Asp Leu Ser Ala Pro Pro Ala Pro Cys Leu Pro Gly Cys
 1 5 10 15
 Arg His Ser Gln His Asp Asp Asn Gly Met Asn Leu Arg Asn Arg Thr
 20 25 30
 Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Asn Ala Leu
 35 40 45
 Glu Glu Lys Glu Asn Lys Ile Val Val Arg Gln Thr Gly Tyr Phe Phe
 50 55 60
 Ile Tyr Ser Gln Val Leu Tyr Thr Asp Pro Ile Phe Ala Met Gly His
 65 70 75 80
 Val Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu
 85 90 95
 Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Lys Thr Leu Pro Asn
 100 105 110
 Asn Ser Cys Tyr Ser Ala Gly Ile Ala Arg Leu Glu Glu Gly Asp Glu
 115 120 125
 Ile Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Arg Asn Gly
 130 135 140
 Asp Asp Thr Phe Phe Gly Ala Leu Lys Leu Leu
 145 150 155

<210> 24

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C

<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer

<400> 24
ccaccagctc caggagaagg caactc

26

<210> 25
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer

<400> 25
accgcgggac tgaaaatct

19

<210> 26
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer

<400> 26
cacgcttatt tctgctgttc tga

23

<210> 27
<211> 657
<212> DNA
<213> Homo sapiens

<400> 27
taccaggtgg cggccgtgca aggggacctg gccagcctcc gggcagagct gcagggccac 60
cacgcggaga agctgccagc aagagcaaga gcccccaagg ccggtctggg ggaagctcca 120
gctgtcaccg caggactgaa aatctttgaa ccaccagctc caggagaagg caactccagt 180
cagagcagca gaaataagcg tgctattcag ggtgcagaag aaacagtcac tcaagactgc 240
ttgcaactga ttgcagacag tgaaacacca actatacaaa aaggatctta cacatttggt 300
ccatggcttc tcagctttaa aaggggaagt gccctagaag aaaaagagaa taaaatattg 360
gtcaaagaaa ctgggtactt ttttatatat ggtcagggtt tatacactga taagacctat 420
gccatgggac atctaattca gaggaaaaaa gtccatgtct ttggggatga attgagctctg 480
gtgactttgt ttcatgtgat tcaaaatatt cctgaaacac tacccaataa ttcctgctat 540
tcagctggca ttgcaaaact ggaagaagga gatgaacttc aacttgcaat accacgagaa 600
aatgcacaaa tatcactgga tggagatgtc acattttttg gtgcctcaa actgctg 657

<210> 28
<211> 219
<212> PRT

<213> Homo sapiens

<400> 28

Tyr Gln Val Ala Ala Val Gln Gly Asp Leu Ala Ser Leu Arg Ala Glu
1 5 10 15

Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Arg Ala Arg Ala Pro
20 25 30

Lys Ala Gly Leu Gly Glu Ala Pro Ala Val Thr Ala Gly Leu Lys Ile
35 40 45

Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Ser Ser Arg
50 55 60

Asn Lys Arg Ala Ile Gln Gly Ala Glu Glu Thr Val Ile Gln Asp Cys
65 70 75 80

Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys Gly Ser
85 90 95

Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu
100 105 110

Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe
115 120 125

Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His
130 135 140

Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu
145 150 155 160

Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn
165 170 175

Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu
180 185 190

Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly
195 200 205

Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
210 215

<210> 29

<211> 657

<212> DNA

<213> Homo sapiens

<400> 29

taccaggtgg cggccgtgca aggggacctg gccagcctcc gggcagagct gcagagccac 60
cacgcgagaga agctgccagc aagagcaaga gcccccaagg ccggtctggg ggaagctcca 120
gctgtcaccg cgggactgaa aatctttgaa ccaccagctc caggagaagg caactccagt 180
cagagcagca gaaataagcg tgctattcag ggtgcagaag aaacagtcac tcaagactgc 240
ttgcaactga ttgcagacag tgaacacca actatacaaa aaggatctta cacatttggt 300
ccatggcttc tcagctttaa aaggggaagt gccctagaag aaaaagagaa taaaatattg 360
gtcaaagaaa ctggttactt ttttatatat gggtcaggtt tatacactga taagacctat 420
gccatgggac atctaattca gaggaacaaa gtccatgtct ttggggatga attgagtctg 480

gtgactttgt ttcgatgtat tcaaaatattg cctgaaacac tacccaataa ttcctgctat 540
 tcagctggca ttgcaaaact ggaagaaggg gatgaacttc aacttgcaat accacgagaa 600
 aatgcacaaa tatcactgga tggagatgtc acattttttg gtgcctcaa actgctg 657

<210> 30
 <211> 219
 <212> PRT
 <213> Homo sapiens

<400> 30
 Tyr Gln Val Ala Ala Val Gln Gly Asp Leu Ala Ser Leu Arg Ala Glu
 1 5 10 15
 Leu Gln Ser His His Ala Glu Lys Leu Pro Ala Arg Ala Arg Ala Pro
 20 25 30
 Lys Ala Gly Leu Gly Glu Ala Pro Ala Val Thr Ala Gly Leu Lys Ile
 35 40 45
 Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Ser Ser Arg
 50 55 60
 Asn Lys Arg Ala Ile Gln Gly Ala Glu Glu Thr Val Ile Gln Asp Cys
 65 70 75 80
 Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys Gly Ser
 85 90 95
 Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu
 100 105 110
 Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe
 115 120 125
 Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His
 130 135 140
 Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu
 145 150 155 160
 Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn
 165 170 175
 Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu
 180 185 190
 Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly
 195 200 205
 Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
 210 215

<210> 31
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>

<221> primer_bind
<223> primer

<400> 31
ggtcgcccgtt tctaacgcgg ccgttcaggg tccagaag

38

<210> 32
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer

<400> 32
ctggttcggc ccaaggtacc aagcttgtag cttagatctt ttctagatc

49

<210> 33
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer

<400> 33
ctggtagttc ttcggagtgt g

21

<210> 34
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer

<400> 34
cgcgtagtaa acggcgacc

19

<210> 35
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer

<220>
<221> misc_feature
<222> (7)
<223> n equals deoxyinosine

C'
cont.

414

C

<220>
<221> misc_feature
<222> (12)
<223> n equals deoxyinosine

<220>
<221> misc_feature
<222> (16)
<223> n equals deoxyinosine

<400> 35
taccagntgg cngccntgca ag

22

<210> 36
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer

<220>
<221> misc_feature
<222> (3)
<223> n equals deoxyinosine

<220>
<221> misc_feature
<222> (14)
<223> n equals deoxyinosine

<220>
<221> misc_feature
<222> (16)..(17)
<223> n equals deoxyinosine

<400> 36
gtnacagcag tttanngca cc

22

<210> 37
<211> 866
<212> DNA
<213> Mus musculus

<400> 37
atggatgagt ctgcaaagac cctgccacca ccgtgcctct gtttttgctc cgagaaagga 60
gaagatatga aagtgggata tgatcccatc actccgcaga aggaggaggg tgctgggttt 120
gggatctgca gggatggaag gctgctggct gctaccctcc tgctggccct gttgtccagc 180
agtttcacag cgatgtcctt gtaccagttg gctgccttgc aagcagacct gatgaacctg 240
cgcattggagc tgcagagcta ccgaggttca gcaacaccag ccgccgcggg tgctccagag 300
ttgaccgctg gagtcaaact cctgacaccg gcagctcctc gaccccacaa ctccagccgc 360
ggccacagga acagacgcgc cttccaggga ccagaggaaa cagaacaaga tgtagacctc 420
tcagctcctc ctgcaccatg cctgcctgga tgccgcatt ctcaacatga tgataatgga 480
atgaacctca gaaacatcat tcaagactgt ctgcagctga ttgcagacag cgacacgccg 540
gccttgaggg agaaagagaa caaaatagtg gtgaggcaaa caggctatct cttcatctac 600
agccagggtt tatacacgga ccccatcttt gctatgggtc atgtcatcca gaggaagaaa 660
gtacacgtct ttggggacga gctgagcctg gtgaccctgt tccgatgtat tcagaatatg 720

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C

cccaaaacac tgcccaacaa ttctgtctac tcggctggca tcgagaggct ggaagaagga 780
 gatgagattc agcttgcaat tcctcgaggag aatgcacaga ttccacgcaa cggagacgac 840
 accttctttg gtgcctaaa actgct 866

<210> 38
 <211> 289
 <212> PRT
 <213> Mus musculus

<400> 38

Met Asp Glu Ser Ala Lys Thr Leu Pro Pro Pro Cys Leu Cys Phe Cys
 1 5 10 15
 Ser Glu Lys Gly Glu Asp Met Lys Val Gly Tyr Asp Pro Ile Thr Pro
 20 25 30
 Gln Lys Glu Glu Gly Ala Trp Phe Gly Ile Cys Arg Asp Gly Arg Leu
 35 40 45
 Leu Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Ser Ser Phe Thr Ala
 50 55 60
 Met Ser Leu Tyr Gln Leu Ala Ala Leu Gln Ala Asp Leu Met Asn Leu
 65 70 75 80
 Arg Met Glu Leu Gln Ser Tyr Arg Gly Ser Ala Thr Pro Ala Ala Ala
 85 90 95
 Gly Ala Pro Glu Leu Thr Ala Gly Val Lys Leu Leu Thr Pro Ala Ala
 100 105 110
 Pro Arg Pro His Asn Ser Ser Arg Gly His Arg Asn Arg Arg Ala Phe
 115 120 125
 Gln Gly Pro Glu Glu Thr Glu Gln Asp Val Asp Leu Ser Ala Pro Pro
 130 135 140
 Ala Pro Cys Leu Pro Gly Cys Arg His Ser Gln His Asp Asp Asn Gly
 145 150 155 160
 Met Asn Leu Arg Asn Ile Ile Gln Asp Cys Leu Gln Leu Ile Ala Asp
 165 170 175
 Ser Asp Thr Pro Ala Leu Glu Glu Lys Glu Asn Lys Ile Val Val Arg
 180 185 190
 Gln Thr Gly Tyr Phe Phe Ile Tyr Ser Gln Val Leu Tyr Thr Asp Pro
 195 200 205
 Ile Phe Ala Met Gly His Val Ile Gln Arg Lys Lys Val His Val Phe
 210 215 220
 Gly Asp Glu Leu Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met
 225 230 235 240
 Pro Lys Thr Leu Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Arg
 245 250 255
 Leu Glu Glu Gly Asp Glu Ile Gln Leu Ala Ile Pro Arg Glu Asn Ala

L116

C

260

265

270

Gln Ile Ser Arg Asn Gly Asp Asp Thr Phe Phe Gly Ala Leu Lys Leu
 275 280 285

Leu

<210> 39

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<221> primer_bind

<223> primer

<400> 39

cagactggat ccgccaccat ggatgactcc acagaaag

38

<210> 40

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<221> primer_bind

<223> primer

<400> 40

cagactggta ccgtcctgcg tgcactacat ggc

33

<210> 41

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<221> primer_bind

<223> primer

<400> 41

tggtgtcttt ctaccaggtg g

21

<210> 42

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<221> primer_bind

<223> primer

<400> 42

tttcttctgg accctgaacg g

21